

SEQUENCE LISTING

<110> RIKEN

<120> A cell death inducing factor, a cell and an animal expressing the same, and a method for screening an anti cell death treating medicament

<130> RFH14-022N

<140>

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<150> JP 2001/294794

<151> 2001-09-26

<160> 4

<170> PatentIn Ver. 2.1

<210> 1

<211> 1768

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (29)..(1405)

<400> 1

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Met Ala Ala Pro Arg Ala Gly Arg

1 5

ggc gca ggc tgg agc ctt cgg gca tgg cgg gct ttg ggg ggc att cgc 100

Gly Ala Gly Trp Ser Leu Arg Ala Trp Arg Ala Leu Gly Gly Ile Arg

10 15 20

tgg ggg agg aga ccc cgt ttg acc cct gac ctc cgg gcc ctg ctg acg 148

Trp Gly Arg Arg Pro Arg Leu Thr Pro Asp Leu Arg Ala Leu Leu Thr

25 30 35 40

tca gga act tct gac ccc cgg gcc cga gtg act tat ggg acc ccc agt 196

Ser Gly Thr Ser Asp Pro Arg Ala Arg Val Thr Tyr Gly Thr Pro Ser

45 50 55

ctc tgg gcc cgg ttg tct gtt ggg gtc act gaa ccc cga gca tgc ctg 244

Leu Trp Ala Arg Leu Ser Val Gly Val Thr Glu Pro Arg Ala Cys Leu

60 65 70

acg tct ggg acc ccg ggt ccc cgg gca caa ctg act gcg gtg acc cca 292

Thr Ser Gly Thr Pro Gly Pro Arg Ala Gln Leu Thr Ala Val Thr Pro

75 80 85

gat acc agg acc cgg gag gcc tca gag aac tct gga acc cgt tcg cgc 340

Asp Thr Arg Thr Arg Glu Ala Ser Glu Asn Ser Gly Thr Arg Ser Arg

90 95 100

gcg tgg ctg gcg gtg gcg ctg ggc gct ggg ggg gca gtg ctg ttg ttg 388

Ala Trp Leu Ala Val Ala Leu Gly Ala Gly Gly Ala Val Leu Leu Leu

105 110 115 120

ttg tgg ggc ggg ggt cggt cct ccgt gcc gtc ctc gcc gcc gtc cct 436
Leu Trp Gly Gly Gly Arg Gly Pro Pro Ala Val Leu Ala Ala Val Pro

125 130 135

agc ccg ccg ccc gct tct ccc cggt agt cag tac aac ttc atc gca gat 484
Ser Pro Pro Pro Ala Ser Pro Arg Ser Gln Tyr Asn Phe Ile Ala Asp

140 145 150

gtg gtg gag aag aca gca cct gcc gtg gtc tat atc gag atc ctg gac 532
Val Val Glu Lys Thr Ala Pro Ala Val Val Tyr Ile Glu Ile Leu Asp

155 160 165

cggt cac cct ttc ttg ggc cgc gag gtc cct atc tcg aac ggc tca gga 580
Arg His Pro Phe Leu Gly Arg Glu Val Pro Ile Ser Asn Gly Ser Gly

170 175 180

ttc gtg gtg gct gcc gat ggg ctc att gtc acc aac gcc cat gtg gtg 628
Phe Val Val Ala Ala Asp Gly Leu Ile Val Thr Asn Ala His Val Val
185 190 195 200

gct gat cggt cgc aga gtc cgt gtg aga ctg cta agc ggc gac acg tat 676
Ala Asp Arg Arg Arg Val Arg Val Arg Leu Leu Ser Gly Asp Thr Tyr
205 210 215

gag gcc gtg gtc aca gct gtg gat ccc gtg gca gac atc gca acg ctg 724
Glu Ala Val Val Thr Ala Val Asp Pro Val Ala Asp Ile Ala Thr Leu
220 225 230

agg att cag act aag gag cct ctc ccc acg ctg cct ctg gga cgc tca 772

Arg Ile Gln Thr Lys Glu Pro Leu Pro Thr Leu Pro Leu Gly Arg Ser

235

240

245

gct gat gtc cgg caa ggg gag ttt gtt gtt gcc atg gga agt ccc ttt 820

Ala Asp Val Arg Gln Gly Glu Phe Val Val Ala Met Gly Ser Pro Phe

250

255

260

gca ctg cag aac acg atc aca tcc ggc att gtt agc tct gct cag cgt 868

Ala Leu Gln Asn Thr Ile Thr Ser Gly Ile Val Ser Ser Ala Gln Arg

265

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275

280

cca gcc aga gac ctg gga ctc ccc caa acc aat gtg gaa tac att caa 916

Pro Ala Arg Asp Leu Gly Leu Pro Gln Thr Asn Val Glu Tyr Ile Gln

285

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act gat gca gct att gat ttt gga aac tct gga ggt ccc ctg gtt aac 964

Thr Asp Ala Ala Ile Asp Phe Gly Asn Ser Gly Gly Pro Leu Val Asn

300

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310

ctg gat ggg gag gtg att gga gtg aac acc atg aag gtc aca gct gga 1012

Leu Asp Gly Glu Val Ile Gly Val Asn Thr Met Lys Val Thr Ala Gly

315

320

325

atc tcc ttt gcc atc cct tct gat cgt ctt cga gag ttt ctg cat cgt 1060

Ile Ser Phe Ala Ile Pro Ser Asp Arg Leu Arg Glu Phe Leu His Arg

330

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340

ggg gaa aag aag aat tcc tcc tcc gga atc agt ggg tcc cag cgg cgc 1108

Gly Glu Lys Lys Asn Ser Ser Ser Gly Ile Ser Gly Ser Gln Arg Arg

345

350

355

360

tac att ggg gtg atg atg ctg acc ctg agt ccc agc atc ctt gct gaa 1156
Tyr Ile Gly Val Met Met Leu Thr Leu Ser Pro Ser Ile Leu Ala Glu

365 370 375

cta cag ctt cga gaa cca agc ttt ccc gat gtt cag cat ggt gta ctc 1204
Leu Gln Leu Arg Glu Pro Ser Phe Pro Asp Val Gln His Gly Val Leu

380 385 390

atc cat aaa gtc atc ctg ggc tcc cct gca cac cgg gct ggt ctg cgg 1252
Ile His Lys Val Ile Leu Gly Ser Pro Ala His Arg Ala Gly Leu Arg

395 400 405

cct ggt gat gtg att ttg gcc att ggg gag cag atg gta caa aat gct 1300
Pro Gly Asp Val Ile Leu Ala Ile Gly Glu Gln Met Val Gln Asn Ala

410 415 420

gaa gat gtt tat gaa gct gtt cga acc caa tcc cag ttg gca gtg cag 1348
Glu Asp Val Tyr Glu Ala Val Arg Thr Gln Ser Gln Leu Ala Val Gln
425 430 435 440

atc cgg cgg gga cga gaa aca ctg acc tta tat gtg acc cct gag gtc 1396
Ile Arg Arg Gly Arg Glu Thr Leu Thr Leu Tyr Val Thr Pro Glu Val
445 450 455

aca gaa tga atagatcacc aagagtatga ggctccctgct ctgatttcct 1445
Thr Glu

ccttgccttt ctggctgagg ttctgagggc accgagacag agggtaaat gaaccagtg 1505

gggcagggtcc ctccaaaccac cagcactgac tcctgggctc tgaagaatca cagaaacact 1565

ttttatataa aataaaatta tacctagcaa catattatag taaaaaatga gggggaggg 1625

cggatcttt tccccacca aaaggctaga ggtaaagctg tatcccccta aacttagggg 1685

agatactgga ctgaccatc ctgaccctt attaaagaaa atgagctgt gccatcttt 1745

gtggcagtt agtcaggtgc tgc 1768

<210> 2

<211> 458

<212> PRT

<213> Homo sapiens

<400> 2

Met Ala Ala Pro Arg Ala Gly Arg Gly Ala Gly Trp Ser Leu Arg Ala

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Trp Arg Ala Leu Gly Gly Ile Arg Trp Gly Arg Arg Pro Arg Leu Thr

20 25 30

Pro Asp Leu Arg Ala Leu Leu Thr Ser Gly Thr Ser Asp Pro Arg Ala

35 40 45

Arg Val Thr Tyr Gly Thr Pro Ser Leu Trp Ala Arg Leu Ser Val Gly

50 55 60

Val Thr Glu Pro Arg Ala Cys Leu Thr Ser Gly Thr Pro Gly Pro Arg

65 70 75 80

Ala Gln Leu Thr Ala Val Thr Pro Asp Thr Arg Thr Arg Glu Ala Ser

85 90 95

Glu Asn Ser Gly Thr Arg Ser Arg Ala Trp Leu Ala Val Ala Leu Gly

100	105	110
Ala Gly Gly Ala Val Leu Leu Leu Leu Trp Gly Gly Gly Arg Gly Pro		
115	120	125
Pro Ala Val Leu Ala Ala Val Pro Ser Pro Pro Pro Ala Ser Pro Arg		
130	135	140
Ser Gln Tyr Asn Phe Ile Ala Asp Val Val Glu Lys Thr Ala Pro Ala		
145	150	155
Val Val Tyr Ile Glu Ile Leu Asp Arg His Pro Phe Leu Gly Arg Glu		
165	170	175
Val Pro Ile Ser Asn Gly Ser Gly Phe Val Val Ala Ala Asp Gly Leu		
180	185	190
Ile Val Thr Asn Ala His Val Val Ala Asp Arg Arg Arg Val Arg Val		
195	200	205
Arg Leu Leu Ser Gly Asp Thr Tyr Glu Ala Val Val Thr Ala Val Asp		
210	215	220
Pro Val Ala Asp Ile Ala Thr Leu Arg Ile Gln Thr Lys Glu Pro Leu		
225	230	235
Pro Thr Leu Pro Leu Gly Arg Ser Ala Asp Val Arg Gln Gly Glu Phe		
245	250	255
Val Val Ala Met Gly Ser Pro Phe Ala Leu Gln Asn Thr Ile Thr Ser		
260	265	270
Gly Ile Val Ser Ser Ala Gln Arg Pro Ala Arg Asp Leu Gly Leu Pro		
275	280	285
Gln Thr Asn Val Glu Tyr Ile Gln Thr Asp Ala Ala Ile Asp Phe Gly		
290	295	300
Asn Ser Gly Gly Pro Leu Val Asn Leu Asp Gly Glu Val Ile Gly Val		
305	310	315
Asn Thr Met Lys Val Thr Ala Gly Ile Ser Phe Ala Ile Pro Ser Asp		
325	330	335
Arg Leu Arg Glu Phe Leu His Arg Gly Glu Lys Lys Asn Ser Ser Ser		

340	345	350
Gly Ile Ser Gly Ser Gln Arg Arg Tyr Ile Gly Val Met Met Leu Thr		
355	360	365
Leu Ser Pro Ser Ile Leu Ala Glu Leu Gln Leu Arg Glu Pro Ser Phe		
370	375	380
Pro Asp Val Gln His Gly Val Leu Ile His Lys Val Ile Leu Gly Ser		
385	390	395
395 400		
Pro Ala His Arg Ala Gly Leu Arg Pro Gly Asp Val Ile Leu Ala Ile		
405	410	415
Gly Glu Gln Met Val Gln Asn Ala Glu Asp Val Tyr Glu Ala Val Arg		
420	425	430
430 435		
Thr Gln Ser Gln Leu Ala Val Gln Ile Arg Arg Gly Arg Glu Thr Leu		
435	440	445
445 450		
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<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic

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<210> 4

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic

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